

Figure 1

Enzyme E1	Enzyme E2	Number of bases selected		Number of potential subgroups (footprints)	
		in the 5' position	in the 3' position		
<u>Bam</u> HI ↓ GGATCC CCTACG	+ <u>Mme</u> I TCCPuAC.....20 AGGPYTG.....18	1/32 (2x4x4)	1/16 (4x4)	16	
<u>Eco</u> RI ↓ GAATTC CTTAAG		1/128 (4x2x4x4)	1/16 (4x4)	16	
<u>Pst</u> I ↓ CTGCAG GACGTC		1/256 (4x4x4x4)	1/256 (4x4x4x4)	256	
<u>Msp</u> I ↓ CCGG GGC	+ <u>Bsm</u> FI GGGAC.....10 CCCTG.....14	1/64 (4x4x4)	1/256 (4x4x4x4)	256	
<u>Xma</u> CI ↓ CCCGGG GGGCC		1/16 (4x4)	1/256 (4x4x4x4)	256	
<u>Msp</u> I ↓ CCGG GGC		1/256 (4x4x4x4)	1/16 (4x4)	16	
<u>Eco</u> 56I ↓ CCCGGC CGGCC	+ <u>Eci</u> I GGCGGA.....11 CCGCCT.....9	1/64 (4x4x4)	1/16 (4x4)	16	
<u>Ksp</u> I ↓ CCGCGG GGCGCC		1/4 (4)	1/16 (4x4)	16	

Figure 2

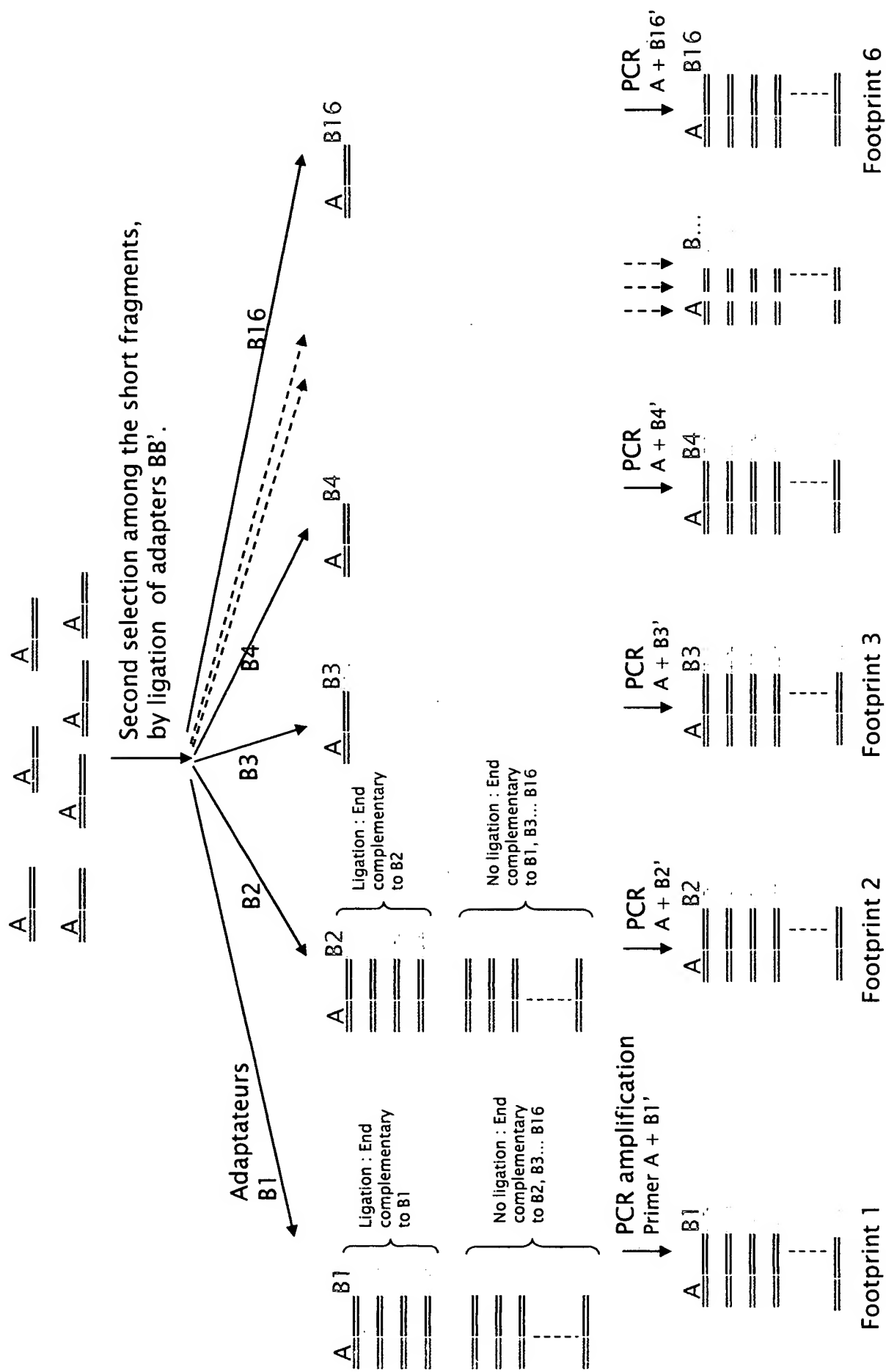


Figure 3

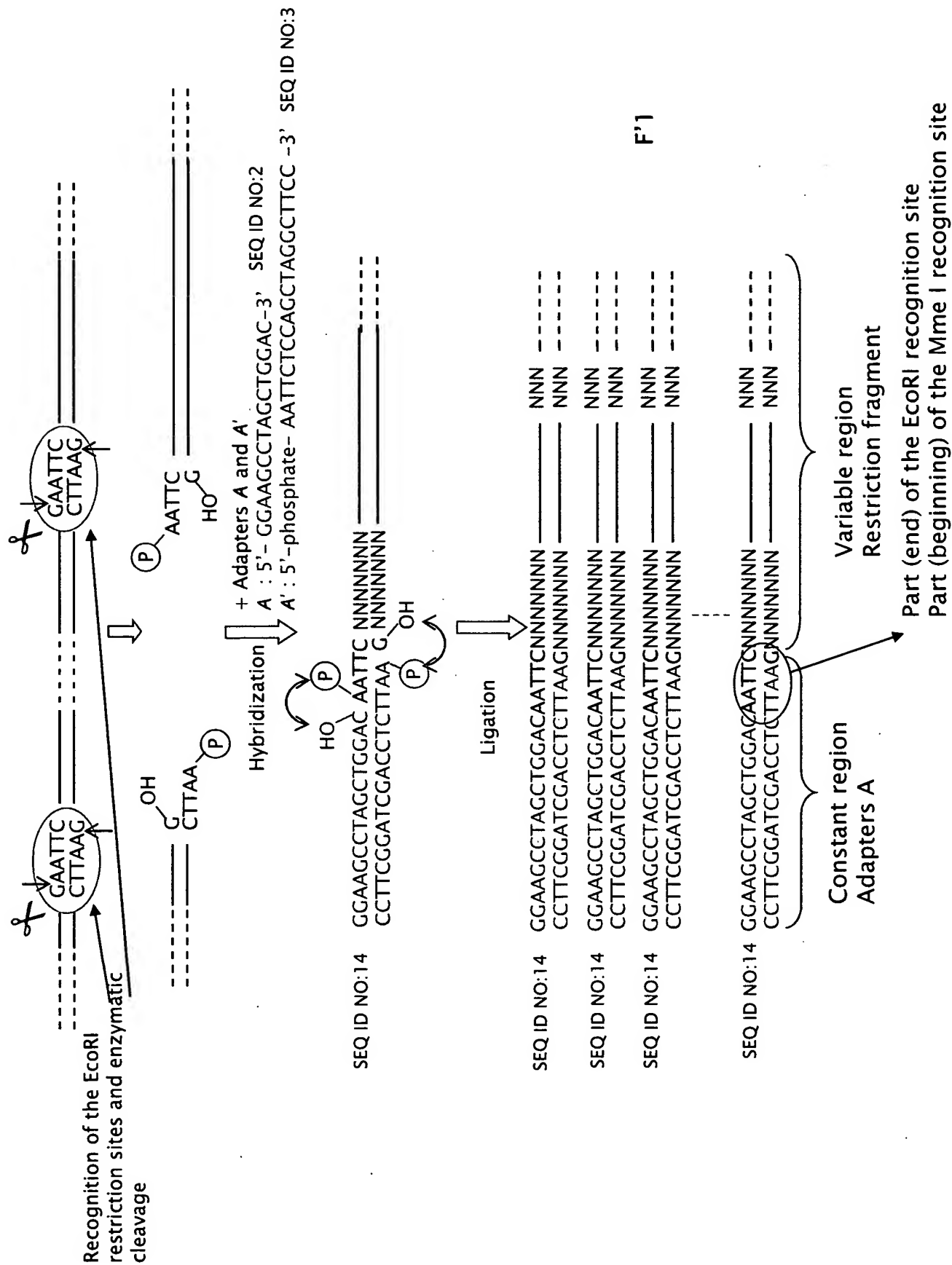


Figure 4-1

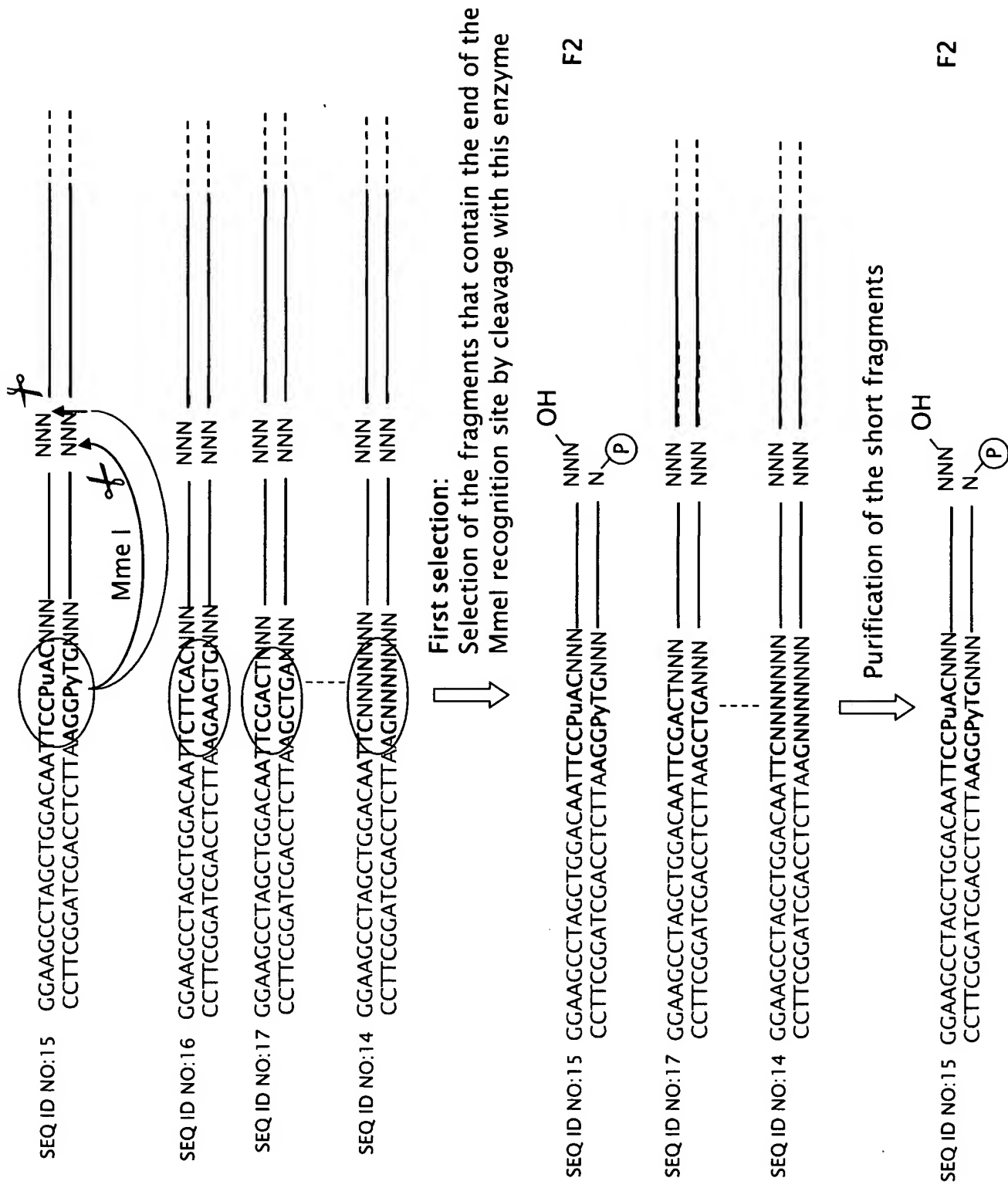


Figure 4-2

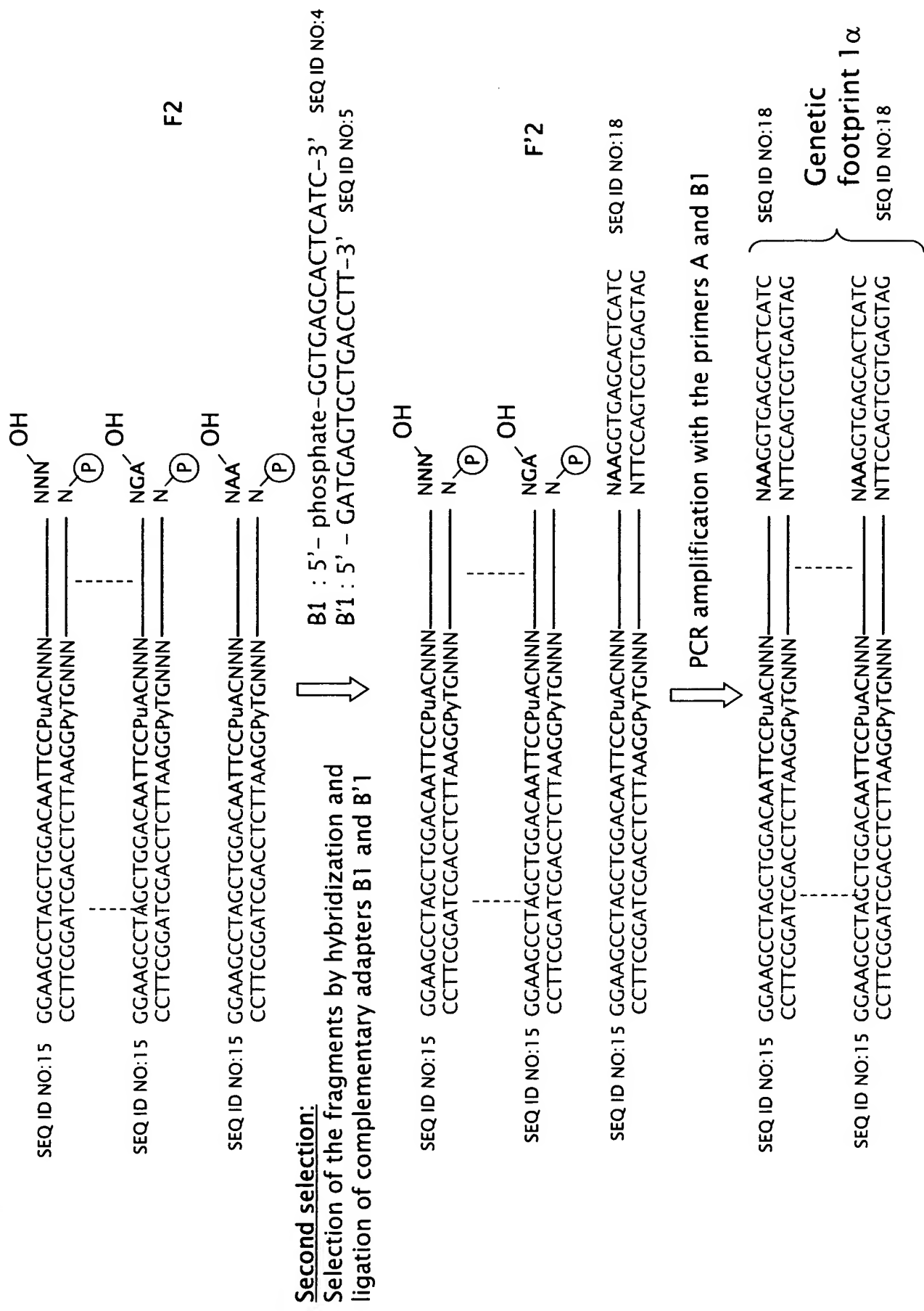


Figure 4-3

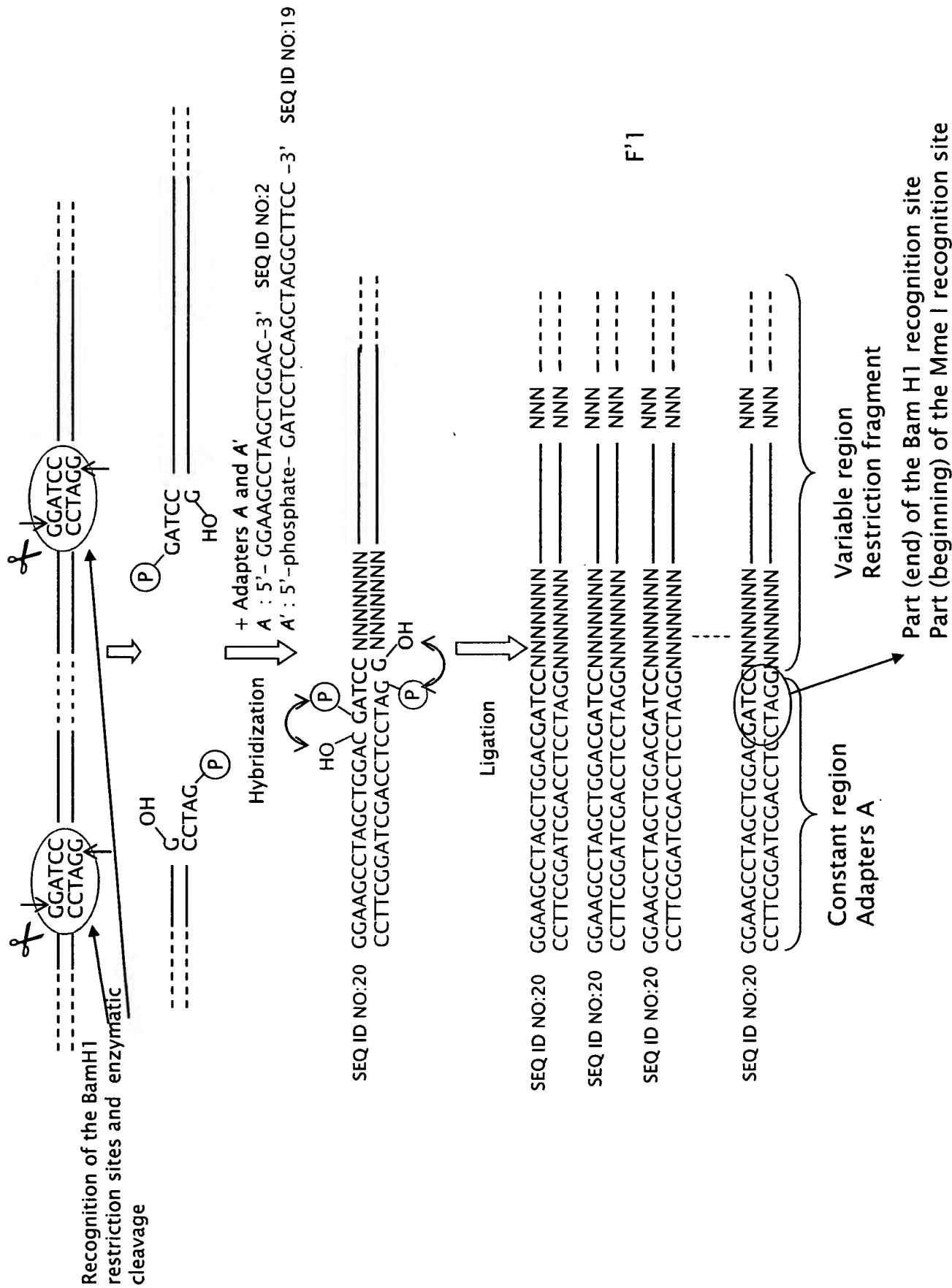


Figure 5-1

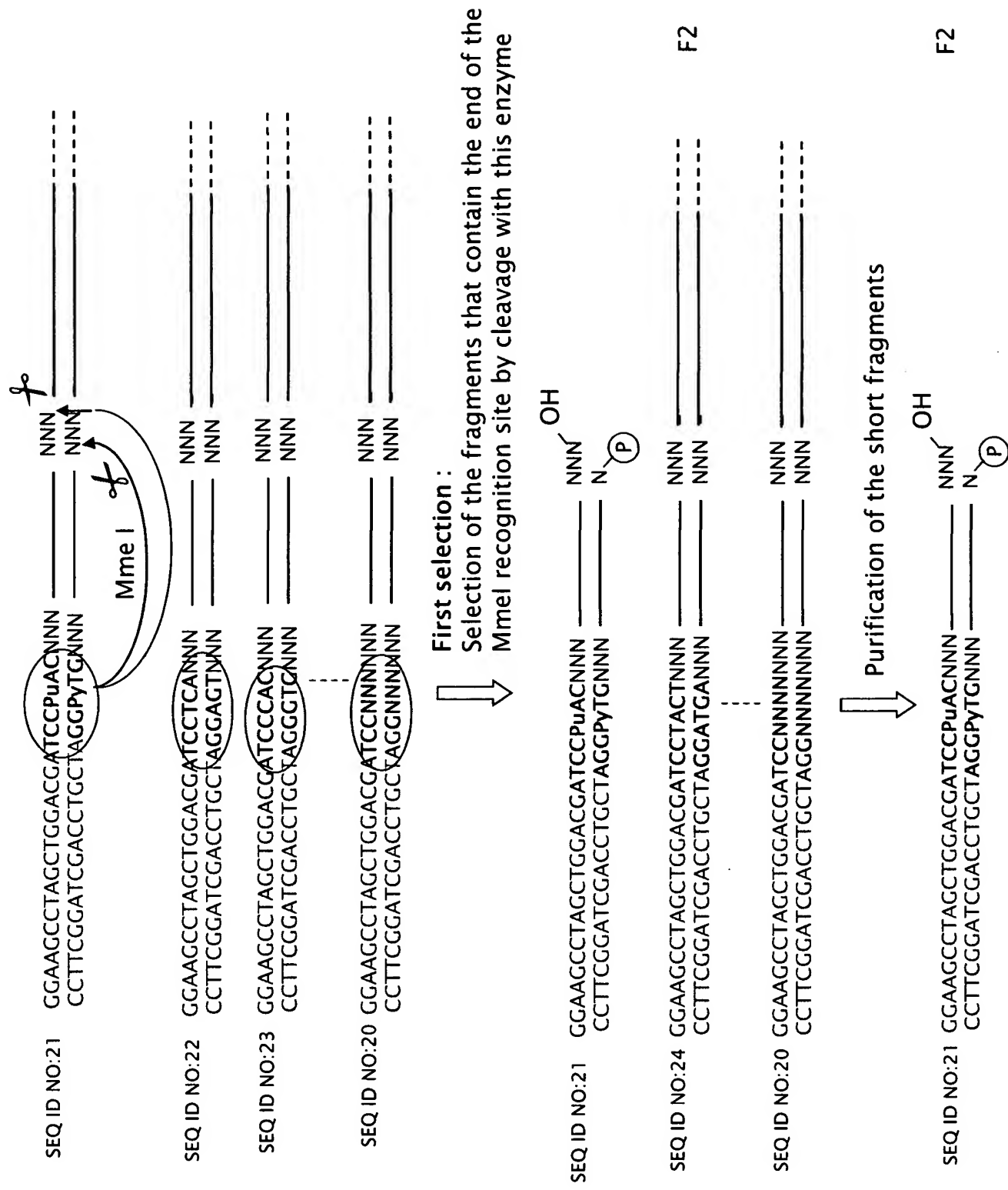


Figure 5-2

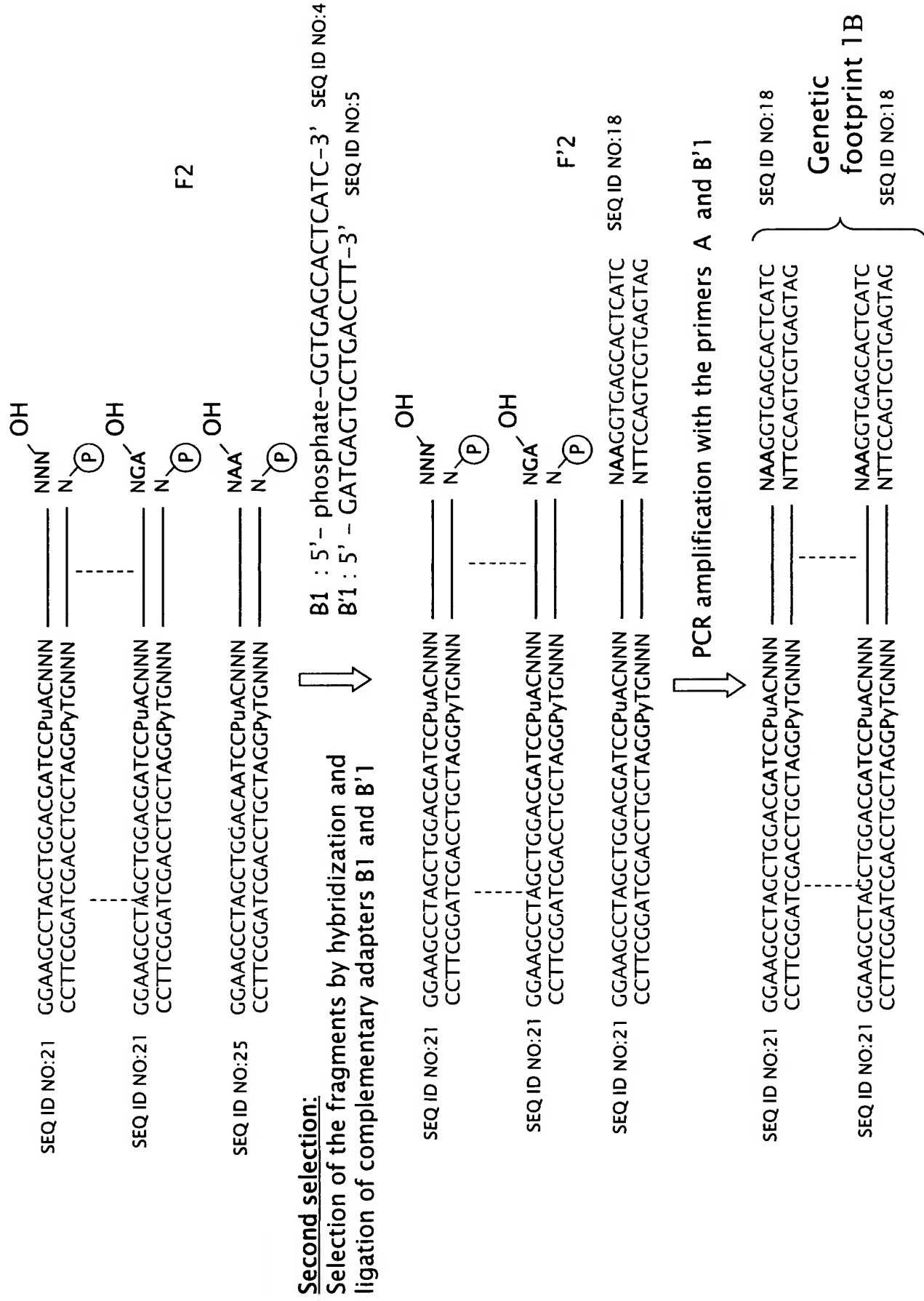


Figure 5-3

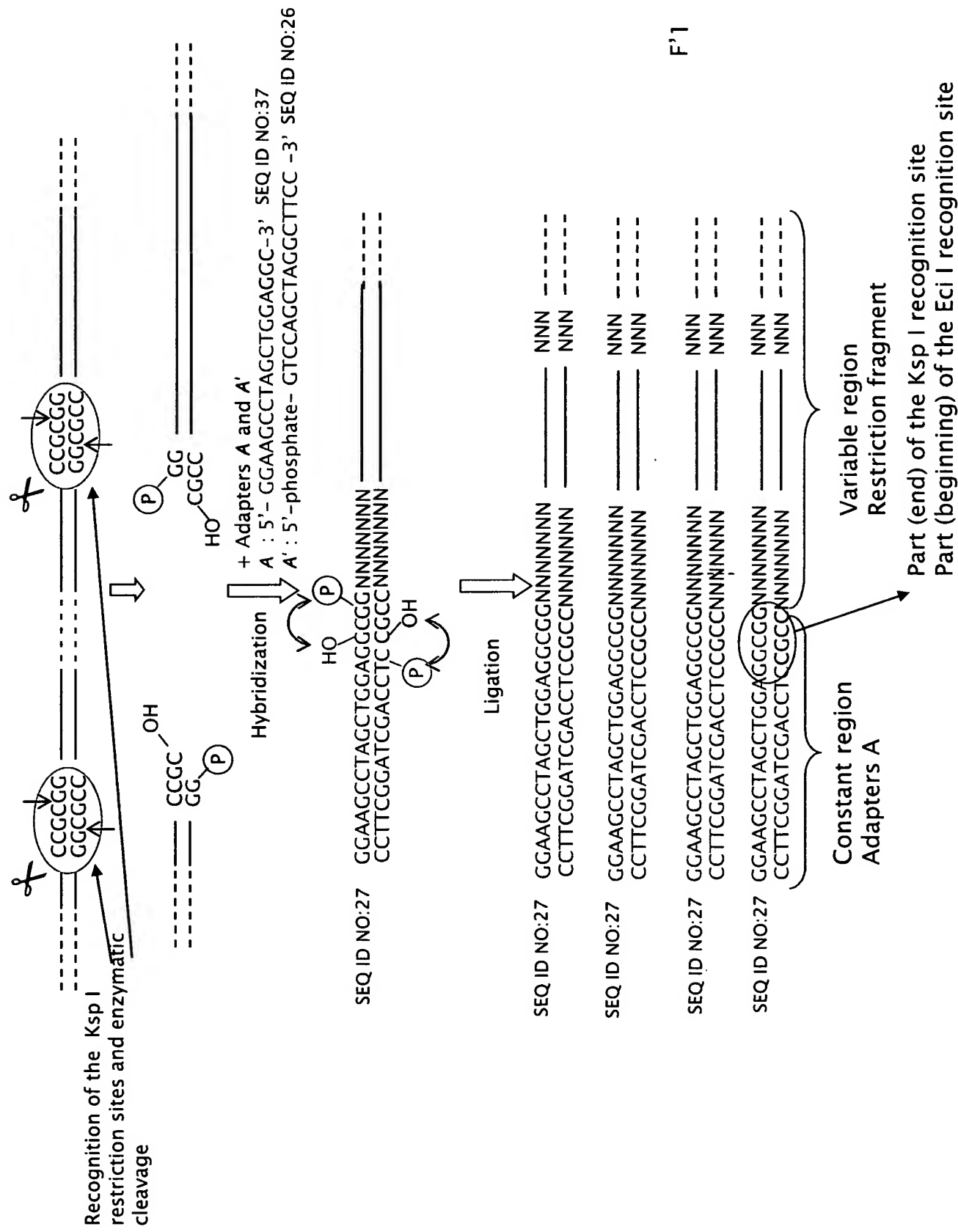


Figure 6-1

SEQ ID NO:28 GGAAGCCTAGCTGGAGCGGANNNNNNN NNN NNN
 CCTTCGGATCGACCT CCGCCTNNNNNN

SEQ ID NO:29 GGAAGCCTAGCTGGAGCGGANNNNNNN NNN NNN
 CCTTCGGATCGACCT CCGCCCNNNNN

SEQ ID NO:30 GGAAGCCTAGCTGGAGCGGTNNNNNNN NNN NNN
 CCTTCGGATCGACCT CCGCCANNNNNN

SEQ ID NO:27 GGAAGCCTAGCTGGAGCGGANNNNNNN NNN NNN
 CCTTCGGATCGACCT CCGCCNNNNNN

Eci I

First selection on one base:
 Selection of the fragments that contain the end of the
 Eci I recognition site by cleavage with this enzyme

SEQ ID NO:28 GGAAGCCTAGCTGGAGCGGANNNNNNN NNN' OH
 CCTTCGGATCGACCT CCGCCTNNNNNN N' (P)

F2

SEQ ID NO:30 GGAAGCCTAGCTGGAGCGGTNNNNNNN NNN NNN
 CCTTCGGATCGACCT CCGCCANNNNNN

SEQ ID NO:27 GGAAGCCTAGCTGGAGCGGANNNNNNN NNN NNN
 CCTTCGGATCGACCT CCGCCNNNNNN

Purification des fragments courts

SEQ ID NO:28 GGAAGCCTAGCTGGAGCGGANNNNNNN NNN' OH
 CCTTCGGATCGACCT CCGCCTNNNNNN N' (P)

F2

Figure 6-2

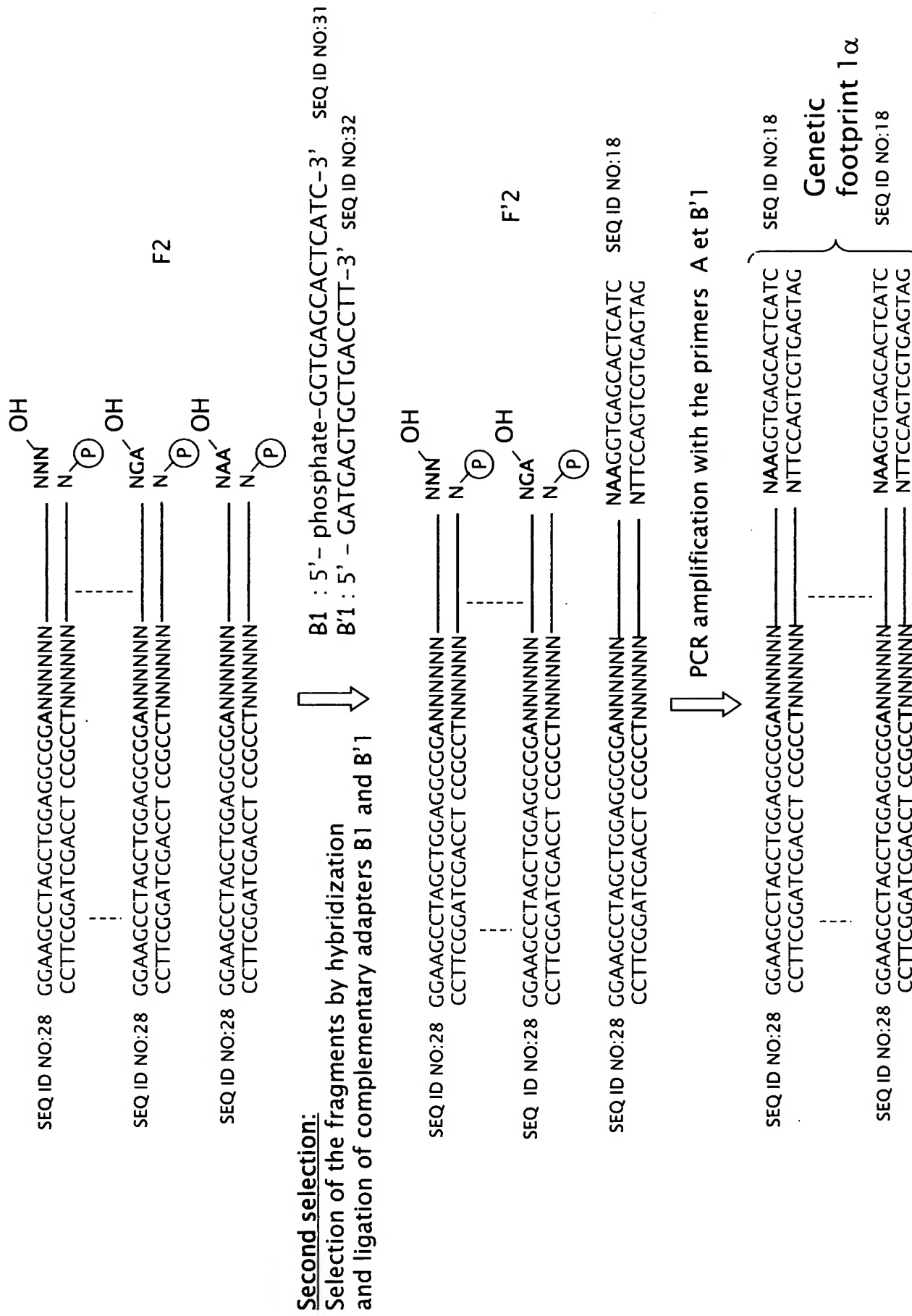


Figure 6-3

7/14

Enzyme E1 _A			Enzyme E2			
Name	Restriction site	Selection 1 of the fragments by cleavage 1 (step a)	Name	Restriction site	Selection 2 of the fragments by cleavage 2 (step c)	Optional selection 3 of the fragments (steps e and f)
<i>Taq^α I</i>	-TCGA -AGCT	governed by E1 _C	<i>BseR I</i>	- <u>GAGGAG</u> N ₁₀ -CTCCTCN ₈ (SEQ ID NO:33)	$\frac{1}{-} = \frac{1}{-}$ 4 ⁴ 256	$\frac{1}{-} = \frac{1}{-}$ 4 ² 16
<i>Msp I</i>	-CCGG -GGCC	governed by E1 _C	<i>BsmF I</i>	- <u>GGGAC</u> N ₁₀ -CCCTGN ₁₄ (SEQ ID NO:34)	$\frac{1}{-} = \frac{1}{-}$ 4 ³ 64	$\frac{1}{-} = \frac{1}{-}$ 4 ⁴ 256
<i>Msp I</i>	-CCGG -GGCC	governed by E1 _C	<i>Eci I</i>	- <u>GGCGG</u> AN ₁₁ -CCGCCTN ₉ (SEQ ID NO:35)	$\frac{1}{-} = \frac{1}{-}$ 4 ⁴ 256	$\frac{1}{-} = \frac{1}{-}$ 4 ² 16
<i>Msp I</i>	-CCGG -GGCC	governed by E1 _C	<i>Fok I</i>	- <u>GGATG</u> N ₉ -CCTACN ₁₃ (SEQ ID NO:36)	$\frac{1}{-} = \frac{1}{-}$ 4 ³ 64	$\frac{1}{-} = \frac{1}{-}$ 4 ⁴ 256

Figure 7